

GenCore version 5.1.4.PS.4578  
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OW protein - protein search, using SW model

Run on: May 23, 2003, 08:00:07, Search time: 11 seconds  
(without alignment)  
101,800 Million pairs of alignments

Title: US-09-897-412-10

Perfect score: 132

Sequence: 1 HSDGFTSELRLRPSARLPILGLSLV 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 11882 seqs, 4145333 pairs

Total number of hits satisfying chosen parameters: 11882

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40

Pred No is the number of residues predicted by the program. A score greater than or equal to the score of the result being printed, and is derived by analysis of the total hits distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	132	100.0	121	SECR_HUMAN
2	126	99.5	27	SECR_CANFA
3	123	99.2	27	SECR_SHEEP
4	123	99.2	131	SECR_PIG
5	119	99.2	134	SECR_RAT
6	113	85.6	133	SECR_MOUSE
7	112	84.8	27	SECR_RABIT
8	78	85.1	27	SECR_CHICK
9	61	46.2	38	SECR_HERGU
10	61	46.2	190	SECR_HAVIR
11	60	45.5	32	SECR_HELIC
12	59	44.7	29	SECR_DIOXA
13	59	44.7	29	SECR_PAPIT
14	59	44.7	73	SECR_GNFA
15	59	44.7	103	SECR_RANCA
16	59	44.7	151	SECR_CHICK
17	59	44.7	158	SECR_PIG
18	59	44.7	190	SECR_POVIN
19	59	44.7	190	SECR_HUMAN
20	59	44.7	190	SECR_HUMAN
21	59	44.7	190	SECR_HUMAN
22	59	44.7	190	SECR_HUMAN
23	59	44.7	190	SECR_HUMAN
24	59	44.7	190	SECR_HUMAN
25	59	44.7	190	SECR_HUMAN
26	59	44.7	190	SECR_HUMAN
27	59	44.7	190	SECR_HUMAN
28	59	44.7	190	SECR_HUMAN
29	59	44.7	190	SECR_HUMAN
30	59	44.7	190	SECR_HUMAN
31	59	44.7	190	SECR_HUMAN
32	59	44.7	190	SECR_HUMAN
33	59	44.7	190	SECR_HUMAN

34	55	41.7	71	SECR_HUMAN
35	55	41.7	71	SECR_HUMAN
36	55	41.7	71	SECR_HUMAN
37	54	40.9	29	SECR_PAPIT
38	54	40.9	29	SECR_PAPIT
39	54	40.9	29	SECR_PAPIT
40	54	40.9	122	SECR_HUMAN
41	53	40.2	29	SECR_HUMAN
42	52	39.4	29	SECR_HUMAN
43	52	39.4	87	SECR_HUMAN
44	52	39.4	87	SECR_HUMAN
45	52	39.4	121	SECR_HUMAN

## ALIGNMENTS

Query Match	100.0%	Score 132	DB ID	Length 101
1	100.0%	132	121	101
2	100.0%	126	27	101
3	100.0%	123	27	101
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6	100.0%	113	133	101
7	100.0%	112	27	101
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9	100.0%	61	38	101
10	100.0%	61	190	101
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32	100.0%	59	190	101
33	100.0%	59	190	101





















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SQ Sequence 27 AA;                                100.0%; Score 132; EG 22; Length 27
Query Match                                     Best Local Similarity 100.0%; Pred. No. 3 Re-Id;
Matches 27 Conservative 0 Mismatches 0 Totals 0 Gaps 0

CY      1 HSDGFSESLPEKAPLPLGLGVY 27          |||||
DB      1 HSDGFTFSELSPLEKARLPGLGLGVY 27    |||||

RESULT 4
ID AAB70890 standard; peptide; 27 AA.
XX AAB70890;
AC AAB70890;
DT 26-JUN-2001 (first entry)
DE Human secretin peptide.
XX Secretin; human; nocotrophic; antistimulatory treatment; prevention
XX Homo sapiens.
XX W02001J32196-A1.
PD 10-MAY-2001.
PF 03-NOV-2000; Z600MT-EPI0847.
XX 05-NOV-1999; 99DE-1053339.
XX (GOLD-) GOLDHAM PHARMMA SWBH.
XX Frank A. Jordan K. Hebel W.
XX MPI; 2001 abstract
XX Pharmacological investigation for inhibition of histamine H2-receptor
XX containing tripeptide fragment having 4-15 preferably 4 or more
XX His-Ser-Asp-Gly-Thr-Phe-Thr-Ser -
PS Disclosure; Page 11; 21pp; German.
XX This invention describes novel pharmaceutical compositions containing at
XX least one secretin peptide fragment having 4-15 preferably 4 or more
XX amino acids particularly in acid addition salt form and which have nutritive
XX activity two peptide fragments described in the invention are any
XX origin, e.g. derived from human, porcine, chicken or other animal
XX have a specific beneficial action in the treatment or prevention of
XX autism They are free of the other activities (e.g. gastrointestinal
XX effects) of secretin itself. This sequence represents the human secretin
XX peptide used to generate the peptide fragments described in the method
XX of the invention.
```

[illegible]

256 The authors are grateful to the referees for their constructive comments and to the  
257 authors of the following papers for their kind suggestions: Peter Breen, David  
258 Griffiths, Robert H. Jones, James K. Mackinnon, James H. Stock, and  
259 International Economic Review, 1990, 31, 1, 1-14; and  
260 Journal of Applied Econometrics, 1990, 5, 1, 1-14.  
261  
262

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W0200010195 A2

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The second element in the first paragraph of the first article of the 1901 constitution is the following: "The Legislature shall have the power to pass laws to regulate the conduct of the courts, and to remove judges from office." This is a very broad and general statement of power, and it is not clear from the text whether it is intended to give the Legislature the power to remove judges from office, or whether it is intended to give the Legislature the power to regulate the conduct of the courts. The text of the constitution is not clear on this point, and it is not clear from the text whether the Legislature has the power to remove judges from office, or whether it is intended to give the Legislature the power to regulate the conduct of the courts.

[illegible][illegible]

Run	Time	Temp	Pressure	Flow	Conc	Yield	Notes
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2	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
3	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
4	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
5	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
6	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
7	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
8	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
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10	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
11	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
12	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
13	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
14	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
15	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
16	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
17	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
18	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
19	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
20	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
21	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
22	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
23	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
24	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
25	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
26	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
27	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
28	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
29	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
30	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
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39	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
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46	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
47	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
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50	10.0	100.0	1.0	1.0	1.0	1.0	Initial run
51	10.0	1					

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2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80																				

[illegible]

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[illegible]

PN JP01144981-A.  
XX  
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[illegible][illegible]





P1 Tsujii M, Hisatake Y, Koitwa A;  
 XX  
 XX WPI: 1982-24132E/13 (24132E).  
 XX  
 XX Hepta-Asa peptide (1) useful for high yield production of high  
 PT purity secretin on strong acid treatment  
 XX  
 XX  
 PS Claim 1; Page 43; 47pp; English.

XX The sequence in AAP0039 is a precursor for the production of  
 CC secretin. The peptide sequences given in AAP0039 are peptides  
 CC which are useful in the production of this precursor. The precursor is  
 CC treated with strong acid in the preparation of secretin. Secretin is  
 CC one of the digestive canal hormones and is useful in the treatment  
 CC of pancreatic external secretion, controlling gastric-stimulating secretion  
 CC of the stomach acid, releasing insulin, stimulating secretion of peptide  
 CC and decomposing fat. It is used as a pancreatic-function examining  
 CC agent and a reagent for testing digestive acids etc.  
 XX  
 SQ Sequence 27 AA;

Query Match 93.2%; Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 7,6e-11;  
 Matches 25; Conservation 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSPREGAPLQPLQGV 27  
 DB 1 HSDGFTSELSPREGAPLQPLQGV 27

## RESULT 13

AAP0021  
 ID AAP0021 standard; peptide; 27 AA

XX  
 XX AAP0021;

XX 03-SEP-1992 (first entry)

XX Synthetic secretin.

XX Pharmacologically: hypersecretion, digestive, hormone production,  
 KW duodenal ulcer.

XX Synthetic.

XX JPS814435-A.

XX 27-ATG-1981.

XX 22-FEB-1992; 927P-007000

XX 22-FEB-1992; 927P-007000

XX (EISA) EISA1 KK.

XX WPI: 1983-779933/40.

XX Pharmacologically active compound in food by removing inhibition

XX gp. from hepatocholepeptide

PS Claim 1; Page 2; 13pp; Japanese.

XX Secretin, which has hitherto been prepared by solid phase synthesis

XX porcine duodenum, may be produced by standard solid phase synthesis.

XX Secretin is a digestive tract hormone with many useful

XX pharmacological actions such as pancreatic secretion promotion,  
 CC gastric stimulation, gastric acid secretion inhibition, insulin  
 CC release, stimulation of peptide secretion and lipolysis activity. It  
 CC is useful as a reagent for test of pancreatic and as a remedy for  
 CC duodenal ulcers.

XX Sequence 27 AA;

Query Match 93.2%; Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 7,6e-11;  
 Matches 25; Conservation 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSPREGAPLQPLQGV 27  
 DB 1 HSDGFTSELSPREGAPLQPLQGV 27

## RESULT 14

AAP0014  
 ID AAP0014 standard; peptide; 27 AA

XX  
 XX AAP0014;

XX 03-SEP-1992 (first entry)

XX 03-SEP-1992 (first entry)

XX Diagnostic, duodenal ulcer, pancreas.

XX Synthetic.

XX JPS720034-A.

XX 08-DEC-1992; 91JP-0094604.

XX 02-JUN-1981; 91JP-0094604.

XX 02-JUN-1981; 91JP-0094604.

XX 01-JAN-1981; 81JP-0084603.

XX 04-FEB-1982; 82JP-0016734.

XX 02-JUN-1981; 81JP-0084604.

XX (EISA) EISA1 KK.

XX WPI: 1983-08056E/04 (08056E).

XX 27 Dec amino secretin EPRD, by recombinant DNA technique

XX useful as diagnostic agent for pancreatic function at that time

XX (first entry) 11-09-81 27 AA

XX Claim 1; Page 1; 15pp; Japanese.

XX Production of the peptide comprises chemical synthesis of the peptide

XX expression gene, introduction of the gene into a plasmid vector,

XX growing in a host microorganism, thereby giving a cultured organism

XX which can grow in the microorganism, transformation of the host cell

XX by the plasmid and cultivation of the resultant transformant and

XX recovery of the peptide. The peptide is useful as a diagnostic

XX agent for pancreatic function and as a drug for treatment of duodenal

XX ulcer. The peptide is useful as a diagnostic agent and a reagent in

XX good yield on large scale with low cost.

XX Sequence 27 AA;

Query Match 93.2%; Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6%; Pred. No. 7,6e-11;  
 Matches 25; Conservation 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSPREGAPLQPLQGV 27  
 DB 1 HSDGFTSELSPREGAPLQPLQGV 27

## RESULT 15

AAP0038  
 ID AAP0038 standard; peptide; 27 AA.

XX  
 XX AAP0038;

XX 04-SEP-1992 (first entry)

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[illegible]



TELEPHONE: 619/576-5337  
TELEFAX: 619/576-5000  
INFORMATION FOR SEQ ID NOS: 36  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-818-253-36

Query Match 93.0%, Score 123, DR 4, Length 27,  
Best Local Similarity 93.0%, Pos 1, Neg 12,  
Matches 25, Conserved 1, Mismatches 1, Indels 0, Gaps 0

QY 1 HSDGTFSELSRPSRARSARLQGLQIV 27  
DB 1 HSDGTFSELSRPSRARSARLQGLQIV 27

RESULT 5  
US-08-818-253-36  
Sequence 36, Application US/0881825336  
Patent No. 6197928

GENERAL INFORMATION:  
APPLICANT: Tesen, Roger Y.  
APPLICANT: Miyawaki, Atsushi  
TITLE OF INVENTION: FLUORESCENT PROTEIN STRUCTURE  
TITLE OF INVENTION: EFFECT OF AMINO ACIDS  
FILE REFERENCE: 07257/042001  
CURRENT APPLICATION NUMBER: US/09/818,253P  
CURRENT FILING DATE: 1997 03 14  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 36  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Sus scrofa  
US-08-818-253-36

Query Match 93.0%, Score 123, DR 4, Length 27,  
Best Local Similarity 93.0%, Pos 1, Neg 12,  
Matches 25, Conserved 1, Mismatches 1, Indels 0, Gaps 0

QY 1 HSDGTFSELSRPSRARSARLQGLQIV 27  
DB 1 HSDGTFSELSRPSRARSARLQGLQIV 27

RESULT 6  
US-09-260-846-12  
Sequence 18, Application US/0926084612  
Patent No. 6307012

GENERAL INFORMATION:  
APPLICANT: QY, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun Hyuk  
TITLE OF INVENTION: OCTAPEPTIDE HOMERIN ANALOGS  
FILE REFERENCE: 00837/009000  
CURRENT APPLICATION NUMBER: US/09/260,846  
CURRENT FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent In Ver 2.1  
SEQ ID NO 18  
LENGTH: 27  
TYPE: PRT  
ORGANISM: mammalian

FEATURE:  
OTHER INFORMATION: Function: Protein  
FEATURE:  
OTHER INFORMATION: This protein has an attached carbohydrate  
US-09-260-846-12

Query Match 93.2%, Score 123, DR 4, Length 27,

Best Local Similarity 93.2%, Pos 1, Neg 12,  
Matches 25, Conserved 1, Mismatches 1, Indels 0, Gaps 0

QY 1 HSDGTFSELSRPSRARSARLQGLQIV 27  
DB 1 HSDGTFSELSRPSRARSARLQGLQIV 27

RESULT 7  
US-08-842-322-30

Sequence 30, Application US/0884232230  
Patent No. 6394058  
GENERAL INFORMATION:  
APPLICANT: Persechini, Anthony  
TITLE OF INVENTION: SELECTION OF CELL CHANGES OF LIGAND  
TITLE OF INVENTION: BINDING BY THE LIGAND PROTEINS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON, HARVEY, CRYSTAL & DYKES LLP  
STREET: Clinton Square, P.O. Box 1951  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
SERIALS: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13  
SOFTWARE: Patent In Release #102, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,322P  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: BERMAN, OSCAR D.  
REGISTRATION NUMBER: 34,103  
REFERENCE/FOREIGN NUMBER: 1/8/00170  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1614  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NOS: 33  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-842-322-30

Query Match 93.2%, Score 123, DR 4, Length 27,  
Best Local Similarity 93.2%, Pos 1, Neg 12,  
Matches 25, Conserved 1, Mismatches 1, Indels 0, Gaps 0

QY 1 HSDGTFSELSRPSRARSARLQGLQIV 27  
DB 1 HSDGTFSELSRPSRARSARLQGLQIV 27

RESULT 8  
US-09-316-913-52

Sequence 52, Application US/0931691352  
Patent No. 6469154  
GENERAL INFORMATION:  
APPLICANT: Tesen, Roger Y.  
APPLICANT: Baird, Geoffrey  
TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS  
FILE REFERENCE: 07257/009000  
CURRENT APPLICATION NUMBER: US/09/316,913P  
CURRENT FILING DATE: 1999 03 21  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52  
LENGTH: 27



## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-0400  
TELEFAX: 202-887-0035

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: YES

US-07-776-272-25

Query Match: 47.0%, Score: 154.5, E: 1e-31, Length: 26,  
Best Local Similarity: 88.9%, Field NO: 126-097,  
Matches: 24, Conservative: 1, Mismatches: 1, Indels: 1, Gaps: 1.

QY 1 HSDGFTSELSPEEAPLQV 27  
DB 1 HSDGFTSELSPEEAPLQV 27

PLT 12  
US-09-303-799D-26

Sequence 26, Application US/09/303799D  
Patent No. 6380357  
GENERAL INFORMATION:

APPLICANT: Hoffmann, Ronald

APPLICANT: Hoffmann, James

FILE REFERENCE: X-10242  
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS

CURRENT FILING DATE: 1999-12-11  
CURRENT APPLICATION NUMBER: US/09/303799D

NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent version 3.0

SEQ ID NO: 26

LENGTH: 31

TYPE: PPT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: synthetic construct

US-09-209-799D-26

Query Match: 47.0%, Score: 154.5, E: 1e-31,  
Best Local Similarity: 44.4%, Field NO: 126-097,  
Matches: 12, Conservative: 4, Mismatches: 9, Indels: 0, Gaps: 0.

QY 1 HSDGFTSELSPEEAPLQV 27  
DB 1 HSDGFTSELSPEEAPLQV 27

RESULT 13  
US-09-303-596-11

Sequence 11, Application US/09/303596-11  
Patent No. 6294722  
GENERAL INFORMATION:

APPLICANT: Ehlert, Thomas E.

APPLICANT: Ehlert, Mario R W.

TITLE OF INVENTION: Methods and compositions for the treatment of

FILE REFERENCE: P03660051  
TITLE OF INVENTION: Methods and compositions for the treatment of

CURRENT FILING DATE: 1999-04-13  
CURRENT APPLICATION NUMBER: US/09/303596-11

PRIOR FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent ver 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Gila monster venom

US-09-303-596-11

Query Match: 46.0%, Score: 154.5, E: 1e-31, Length: 37,  
Best Local Similarity: 44.4%, Field NO: 3017,  
Matches: 12, Conservative: 6, Mismatches: 9, Indels: 0, Gaps: 0.

QY 1 HSDGFTSELSPEEAPLQV 27  
DB 1 HSDGFTSELSPEEAPLQV 27

RESULT 14  
US-09-303-415-11

Sequence 11, Application US/09/303415-11  
Patent No. 641180  
GENERAL INFORMATION:

APPLICANT: Holst, Jens O.

APPLICANT: Valicelli, Tina

TITLE OF INVENTION: GLP-1 as a Diagnostic Test to Determine Gut Health

TITLE OF INVENTION: Methods and compositions for the treatment of

FILE REFERENCE: P03960050  
TITLE OF INVENTION: Methods and compositions for the treatment of

CURRENT FILING DATE: 1999-06-15  
CURRENT APPLICATION NUMBER: US/09/303415-11

NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent ver 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Helicobacter

US-09-303-415-11

Query Match: 46.0%, Score: 154.5, E: 1e-31, Length: 37,  
Best Local Similarity: 44.4%, Field NO: 3017,  
Matches: 12, Conservative: 6, Mismatches: 9, Indels: 0, Gaps: 0.

QY 1 HSDGFTSELSPEEAPLQV 27  
DB 1 HSDGFTSELSPEEAPLQV 27

RESULT 15  
US-09-303-016-11

Sequence 11, Application US/09/303016-11  
Patent No. 632197  
GENERAL INFORMATION:

APPLICANT: Ehlert, Thomas E.

APPLICANT: Ehlert, Mario R W.

TITLE OF INVENTION: Methods and compositions for the treatment of

TITLE OF INVENTION: Active Analgesics for Treating the Symptoms of

FILE REFERENCE: P03660052  
TITLE OF INVENTION: Methods and compositions for the treatment of

CURRENT FILING DATE: 1999-04-13  
CURRENT APPLICATION NUMBER: US/09/303016-11

PRIOR FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent ver 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Helicobacter

US-09-303-016-11

Query Match: 46.0%, Score: 154.5, E: 1e-31, Length: 37,  
Best Local Similarity: 44.4%, Field NO: 3017,  
Matches: 12, Conservative: 6, Mismatches: 9, Indels: 0, Gaps: 0.

QY 1 HSDGFTSELSPEEAPLQV 27  
DB 1 HSDGFTSELSPEEAPLQV 27

Tue May 27 13:06:14 2003

us-09-897-412-10.rai

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US-09-847-249A-28  
; Sequence 28, Application US/8997249A  
; Publication No. US2003022588A1  
; GENERAL INFORMATION:  
; APPLICANT: MARSHALL, WILLIAM S.  
; APPLICANT: STARK, KEVIN LEE  
; TITLE OF INVENTION: GUTACON ANTAGONIST  
; FILE REFERENCE: A-693  
; CURRENT APPLICATION NUMBER: US/09/847,249A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,436  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: ParentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Gutagon Antagonist  
; NAME/KEY: misc.feature  
; LOCATION: (21)..(21)  
; OTHER INFORMATION: Xaa is norleucine (Nle)  
09-847-249A-28

Query Match 47.7%, Score 63, DB 3, Length 29,  
Best Local Similarity 48.1%, Pred. No. 0.01,  
Matches 13, Conservative 4, Mismatches 10, Indels 0  
QY 1 HSGFTSELSRLEFVAPLQELGLV 27  
||| ||||| : ||| :  
EQ 1 HSGFTSEYSKYLDSRAQYFQWIM 27

Search completed: May 23, 2003, 09:04:09  
Job time: 17 secs













Tue May 27 13:06:15 2003

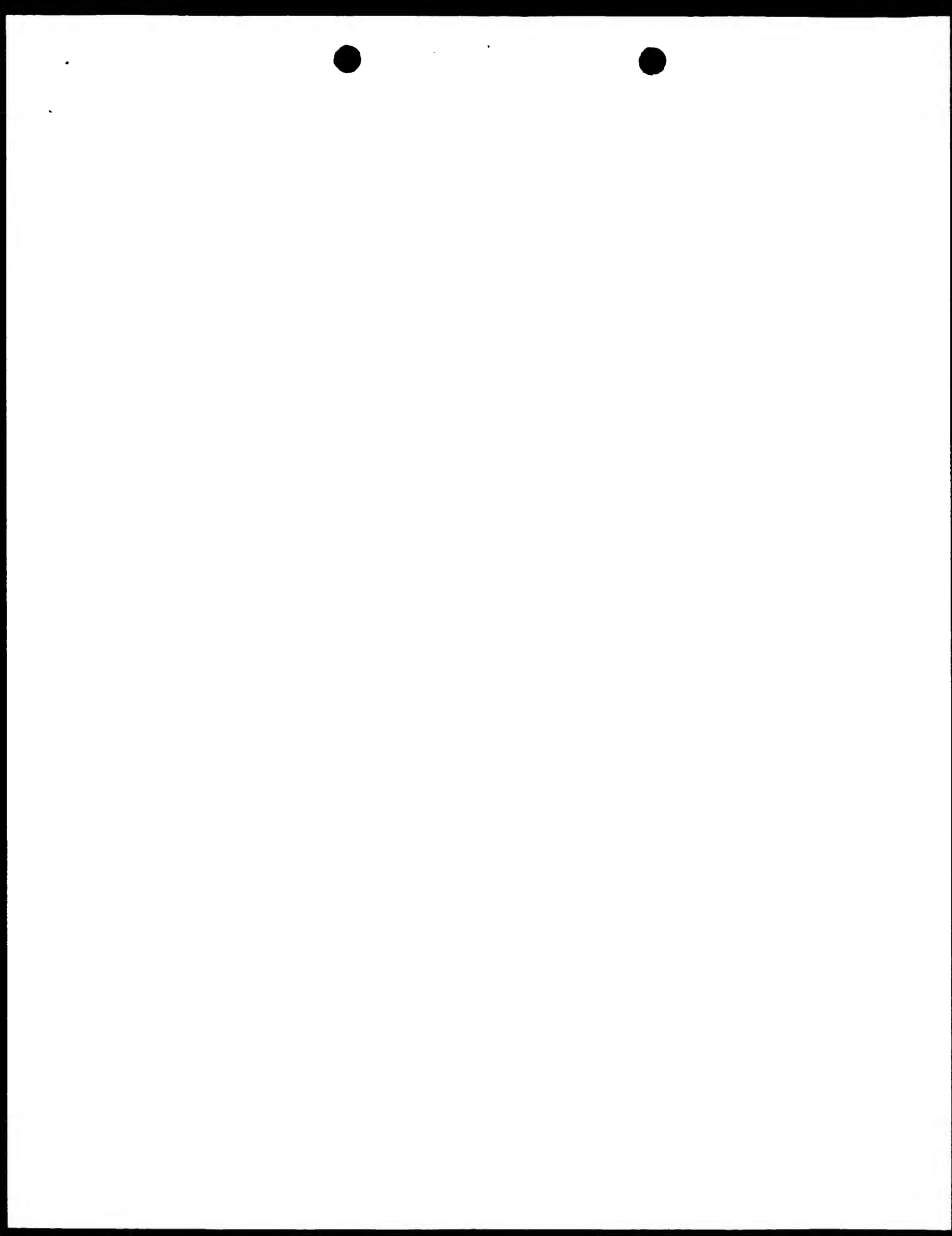
us-09-897-412-10.rpr

Page 5

Best Local Similarity 44.4%; Pred No 0.019;  
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 HSDGFTSELSPFPGAPLQPLQSLV 27  
| | | | | : : : : :  
Db 1 HSGGFTSDYSKYLDSRPAQDFVQWLM 27

Search completed: May 23, 2003, 09:03:24  
Job time : 17 secs













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12	24	36
18	30	42
24	36	48
30	42	54
36	48	60
42	54	66
48	60	72
54	66	78
60	72	84
66	78	90
72	84	96
78	90	102
84	96	108
90	102	114
96	108	120
102	114	126
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252	264	276
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264	276	288
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660	672	684
666	678	690
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678	690	702
684	696	708
690	702	714
696	708	720
702	714	726
708	720	732
714	726	738
720		

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Figure 1 is a schematic representation of the experimental design. It shows a sequence of four boxes: 'Stimulus', 'Response', 'Feedback', and 'Outcome'. Arrows connect these boxes in sequence. A legend indicates that a solid line represents 'Correct' and a dashed line represents 'Incorrect'.

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